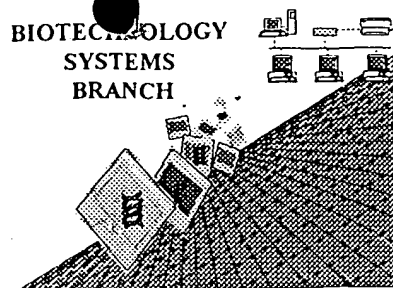


## RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/781, 712 A

Source: 1635

Date Processed by STIC: 5-17-01

RECEIVED

JUN 04 2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/781,712 A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length      Sequence(s) ☐ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ☐. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES)      Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES)      Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10 ☐ Use of n's or Xaa's (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☒ Use of "Artificial" (NEW RULES)      Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.  
Valid response is Artificial Sequence.
- 12 ☐ Use of <220>Feature (NEW RULES)      Sequence(s) ☐ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown".  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1635

## RAW SEQUENCE LISTING

DATE: 05/17/2001

PATENT APPLICATION: US/09/781,712A

TIME: 10:13:22

Input Set : A:\es.txt

Output Set: N:\CRF3\05172001\I781712A.raw

Does Not Comply  
Corrected Diskette Needed  
See pp 5-6

```

5 <110> APPLICANT: Crooke, Stanley T.
6   Lima, Walter
7   Wu, Hongjiang
9 <120> TITLE OF INVENTION: Methods of Using Mammalian RNase H and Compositions Thereof
12 <130> FILE REFERENCE: ISPH-0520
14 <140> CURRENT APPLICATION NUMBER: US/09/781,712A
15 <141> CURRENT FILING DATE: 2001-02-12
17 <150> PRIOR APPLICATION NUMBER: US 09/684,254
18 <151> PRIOR FILING DATE: 2000-10-06
21 <150> PRIOR APPLICATION NUMBER: US 09/343,809
22 <151> PRIOR FILING DATE: 1999-06-30
25 <150> PRIOR APPLICATION NUMBER: US 09/203,716
26 <151> PRIOR FILING DATE: 1998-12-02
29 <150> PRIOR APPLICATION NUMBER: US 60/067,458
30 <151> PRIOR FILING DATE: 1997-12-04
33 <160> NUMBER OF SEQ ID NOS: 39
36 <170> SOFTWARE: PatentIn version 3.0
39 <210> SEQ ID NO: 1
41 <211> LENGTH: 299
43 <212> TYPE: PRT
45 <213> ORGANISM: Homo sapiens
49 <400> SEQUENCE: 1
51 Met Asp Leu Ser Glu Leu Glu Arg Asp Asn Thr Gly Arg Cys Arg Leu
52 1           5           10           15
54 Ser Ser Pro Val Pro Ala Val Cys Arg Lys Glu Pro Cys Val Leu Gly
55           20           25           30
57 Val Asp Glu Ala Gly Arg Gly Pro Val Leu Gly Pro Met Val Tyr Ala
58           35           40           45
60 Ile Cys Tyr Cys Pro Leu Pro Arg Leu Ala Asp Leu Glu Ala Leu Lys
61           50           55           60
63 Val Ala Asp Ser Lys Thr Leu Leu Glu Ser Glu Arg Glu Arg Leu Phe
64 65           70           75           80
66 Ala Lys Met Glu Asp Thr Asp Phe Val Gly Trp Ala Leu Asp Val Leu
67           85           90           95
69 Ser Pro Asn Leu Ile Ser Thr Ser Met Leu Gly Trp Val Lys Tyr Asn
70           100          105          110
72 Leu Asn Ser Leu Ser His Asp Thr Ala Thr Gly Leu Ile Gln Tyr Ala
73           115          120          125
75 Leu Asp Gln Gly Val Asn Val Thr Gln Val Phe Val Asp Thr Val Gly
76           130          135          140
78 Met Pro Glu Thr Tyr Gln Ala Arg Leu Gln Gln Ser Phe Pro Gly Ile
79 145          150          155          160
81 Glu Val Thr Val Lys Ala Lys Ala Asp Ala Leu Tyr Pro Val Val Ser
82           165          170          175
84 Ala Ala Ser Ile Cys Ala Lys Val Ala Arg Asp Gln Ala Val Lys Lys
85           180          185          190
87 Trp Gln Phe Val Glu Lys Leu Gln Asp Leu Asp Thr Asp Tyr Gly Ser

```

## RAW SEQUENCE LISTING

DATE: 05/17/2001

PATENT APPLICATION: US/09/781,712A

TIME: 10:13:22

Input Set : A:\es.txt

Output Set: N:\CRF3\05172001\I781712A.raw

```

88      195      200      205
90 Gly Tyr Pro Asn Asp Pro Lys Thr Lys Ala Trp Leu Lys Glu His Val
91      210      215      220
93 Glu Pro Val Phe Gly Phe Pro Gln Phe Val Arg Phe Ser Trp Arg Thr
94 225      230      235      240
96 Ala Gln Thr Ile Leu Glu Lys Glu Ala Glu Asp Val Ile Trp Glu Asp
97      245      250      255
99 Ser Ala Ser Glu Asn Gln Glu Gly Leu Arg Lys Ile Thr Ser Tyr Phe
100      260      265      270
102 Leu Asn Glu Gly Ser Gln Ala Arg Pro Arg Ser Ser His Arg Tyr Phe
103      275      280      285
105 Leu Glu Arg Gly Leu Glu Ser Ala Thr Ser Leu
106      290      295
108 <210> SEQ ID NO: 2
110 <211> LENGTH: 128
112 <212> TYPE: PRT
114 <213> ORGANISM: Mus sp.
118 <400> SEQUENCE: 2
120 Met Asp Leu Ser Glu Leu Glu Arg Asp Asn Thr Gly Arg Cys Arg Leu
121 1      5      10      15
123 Ser Ser Pro Val Pro Ala Val Cys Leu Lys Glu Pro Cys Val Leu Gly
125      20      25      30
127 Val Asp Glu Ala Gly Arg Gly Pro Val Leu Gly Pro Met Val Tyr Ala
128      35      40      45
130 Ile Cys Tyr Cys Pro Leu Ser Arg Leu Ala Asp Leu Glu Ala Leu Lys
131      50      55      60
133 Val Ala Asp Ser Lys Thr Leu Thr Glu Asn Glu Arg Glu Arg Leu Phe
134 65      70      75      80
136 Ala Lys Met Glu Glu Asp Gly Asp Phe Val Gly Trp Ala Leu Asp Val
137      85      90      95
139 Leu Ser Pro Asn Leu Ile Ser Thr Ser Met Leu Gly Arg Val Lys Tyr
140      100      105      110
142 Asn Leu Asn Ser Leu Ser His Asp Thr Ala Ala Gly Leu Ile Gln Tyr
143      115      120      125
145 <210> SEQ ID NO: 3
147 <211> LENGTH: 307
149 <212> TYPE: PRT
151 <213> ORGANISM: Caenorhabditis elegans
155 <400> SEQUENCE: 3
157 Ser Lys Thr Val Lys Tyr Phe Ile Glu Arg Met Ser Leu Lys Cys Glu
158 1      5      10      15
160 Thr Glu Arg Ser Lys Thr Trp Asn Asn Phe Gly Asn Gly Ile Pro Cys
161      20      25      30
163 Val Leu Gly Ile Asp Glu Ala Gly Arg Gly Pro Val Leu Gly Pro Met
164      35      40      45
166 Val Tyr Ala Ala Ala Ile Ser Pro Leu Asp Gln Asn Val Glu Leu Lys
167      50      55      60
169 Asn Leu Gly Val Asp Asp Ser Lys Ala Leu Asn Glu Ala Lys Arg Glu
170 65      70      75      80

```

## RAW SEQUENCE LISTING

DATE: 05/17/2001

PATENT APPLICATION: US/09/781,712A

TIME: 10:13:22

Input Set : A:\es.txt

Output Set: N:\CRF3\05172001\I781712A.raw

```

172 Glu Ile Phe Asn Lys Met Asn Glu Asp Glu Asp Ile Gln Gln Ile Ile
173      85      90      95
175 Ala Tyr Ala Leu Arg Cys Leu Ser Pro Glu Leu Ile Ser Cys Ser Met
176      100     105     110
178 Leu Lys Arg Gln Lys Tyr Ser Leu Asn Glu Val Ser His Glu Ala Ala
179      115     120     125
181 Ile Thr Leu Ile Arg Asp Ala Leu Ala Cys Asn Val Asn Val Val Glu
182      130     135     140
184 Ile Lys Val Asp Thr Val Gly Pro Lys Ala Thr Tyr Gln Ala Lys Leu
185 145      150     155     160
187 Glu Lys Leu Phe Pro Gly Ile Ser Ile Cys Val Thr Glu Lys Ala Asp
188      165     170     175
190 Ser Leu Phe Pro Ile Val Ser Ala Ala Ser Ile Ala Ala Lys Val Thr
191      180     185     190
193 Arg Asp Ser Arg Leu Arg Asn Trp Gln Phe Arg Glu Lys Asn Ile Lys
194      195     200     205
196 Val Pro Asp Ala Gly Tyr Gly Ser Gly Tyr Pro Gly Asp Pro Asn Thr
197      210     215     220
199 Lys Lys Phe Leu Gln Leu Ser Val Glu Pro Val Phe Gly Phe Cys Ser
200 225      230     235     240
202 Leu Val Arg Ser Ser Trp Lys Thr Ala Ser Thr Ile Val Glu Lys Arg
203      245     250     255
205 Cys Val Pro Gly Ser Trp Glu Asp Asp Glu Glu Glu Gly Lys Ser Gln
206      260     265     270
208 Ser Lys Arg Met Thr Ser Trp Met Val Pro Lys Asn Glu Thr Glu Val
209      275     280     285
211 Val Pro Lys Arg Asn Met Glu Ile Asn Leu Thr Lys Ile Val Ser Thr
212      290     295     300
214 Leu Phe Leu
215 305
217 <210> SEQ ID NO: 4
219 <211> LENGTH: 307
221 <212> TYPE: PRT
223 <213> ORGANISM: Saccharomyces cerevisiae
227 <400> SEQUENCE: 4
229 Met Val Pro Pro Thr Val Glu Ala Ser Leu Glu Ser Pro Tyr Thr Lys
230 1      5      10      15
232 Ser Tyr Phe Ser Pro Val Pro Ser Ala Leu Leu Glu Gln Asn Asp Ser
233      20      25      30
235 Pro Ile Ile Met Gly Ile Asp Glu Ala Gly Arg Gly Pro Val Leu Gly
236      35      40      45
238 Pro Met Val Tyr Ala Val Ala Tyr Ser Thr Gln Lys Tyr Gln Asp Glu
239      50      55      60
241 Thr Ile Ile Pro Asn Tyr Glu Phe Asp Asp Ser Lys Lys Leu Thr Asp
242 65      70      75      80
244 Pro Ile Arg Arg Met Leu Phe Ser Lys Ile Tyr Gln Asp Asn Glu Glu
245      85      90      95
247 Leu Thr Gln Ile Gly Tyr Ala Thr Thr Cys Ile Thr Pro Leu Asp Ile
249      100     105     110

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/781,712A

DATE: 05/17/2001

TIME: 10:13:22

Input Set : A:\es.txt

Output Set: N:\CRF3\05172001\I781712A.raw

```

251 Ser Arg Gly Met Ser Lys Phe Pro Pro Thr Arg Asn Tyr Asn Leu Asn
252      115      120      125
254 Glu Gln Ala His Asp Val Thr Met Ala Leu Ile Asp Gly Val Ile Lys
255      130      135      140
257 Gln Asn Val Lys Leu Ser His Val Tyr Val Asp Thr Val Gly Pro Pro
258 145      150      155      160
260 Ala Ser Tyr Gln Lys Lys Leu Glu Gln Arg Phe Pro Gly Val Lys Phe
261      165      170      175
263 Thr Val Ala Lys Lys Ala Asp Ser Leu Tyr Cys Met Val Ser Val Ala
264      180      185      190
266 Ser Val Val Ala Lys Val Thr Arg Asp Ile Leu Val Glu Ser Leu Lys
267      195      200      205
269 Arg Asp Pro Asp Glu Ile Leu Gly Ser Gly Tyr Pro Ser Asp Pro Lys
270      210      215      220
272 Thr Val Ala Trp Leu Lys Arg Asn Gln Thr Ser Leu Met Gly Trp Pro
273 225      230      235      240
275 Ala Asn Met Val Arg Phe Ser Trp Gln Thr Cys Gln Thr Leu Leu Asp
276      245      250      255
278 Asp Ala Ser Lys Asn Ser Ile Pro Ile Lys Trp Glu Glu Gln Tyr Met
279      260      265      270
281 Asp Ser Arg Lys Asn Ala Ala Gln Lys Thr Lys Gln Leu Gln Leu Gln
282      275      280      285
284 Met Val Ala Lys Pro Val Arg Arg Lys Arg Leu Arg Thr Leu Asp Asn
285      290      295      300
287 Trp Tyr Arg
288 305
290 <210> SEQ ID NO: 5
292 <211> LENGTH: 198
294 <212> TYPE: PRT
296 <213> ORGANISM: Escherichia coli
300 <400> SEQUENCE: 5
302 Met Ile Glu Phe Val Tyr Pro His Thr Gln Leu Val Ala Gly Val Asp
303 1      5      10      15
305 Glu Val Gly Arg Gly Pro Leu Val Gly Ala Val Val Thr Ala Ala Val
306      20      25      30
308 Ile Leu Asp Pro Ala Arg Pro Ile Ala Gly Leu Asn Asp Ser Lys Lys
309      35      40      45
311 Leu Ser Glu Lys Arg Arg Leu Ala Leu Tyr Glu Glu Ile Lys Glu Lys
312      50      55      60
314 Ala Leu Ser Trp Ser Leu Gly Arg Ala Glu Pro His Glu Ile Asp Glu
315 65      70      75      80
317 Leu Asn Ile Leu His Ala Thr Met Leu Ala Met Gln Arg Ala Val Ala
318      85      90      95
320 Gly Leu His Ile Ala Pro Glu Tyr Val Leu Ile Asp Gly Asn Arg Cys
321      100      105      110
323 Pro Lys Leu Pro Met Pro Ala Met Ala Val Val Lys Gly Asp Ser Arg
324      115      120      125
326 Val Pro Glu Ile Ser Ala Ala Ser Ile Leu Ala Lys Val Thr Arg Asp
327      130      135      140

```

## RAW SEQUENCE LISTING

DATE: 05/17/2001

PATENT APPLICATION: US/09/781,712A

TIME: 10:13:22

Input Set : A:\es.txt

Output Set: N:\CRF3\05172001\I781712A.raw

329 Ala Glu Met Ala Ala Leu Asp Ile Val Phe Pro Gln Tyr Gly Phe Ala  
 330 145 150 155 160  
 332 Gln His Lys Gly Tyr Pro Thr Ala Phe His Leu Glu Lys Leu Ala Glu  
 333 165 170 175  
 335 His Gly Ala Thr Glu His His Arg Arg Ser Phe Gly Pro Val Lys Arg  
 336 180 185 190  
 338 Ala Leu Gly Leu Ala Ser  
 339 195  
 341 <210> SEQ ID NO: 6  
 343 <211> LENGTH: 286  
 345 <212> TYPE: PRT  
 347 <213> ORGANISM: Homo sapiens  
 351 <300> PUBLICATION INFORMATION:  
 353 <302> TITLE: Human Type 2 RNase H  
 W--> 355 ~~<309> DATABASE ENTRY DATE:~~  
 W--> 357 <310> PATENT DOC NO: US/09/203,726  
 359 <311> PATENT FILING DATE: 1998-12-02  
 361 <312> PUBLICATION DATE: 1999-12-14  
 365 <400> SEQUENCE: 6  
 367 Met Ser Trp Leu Leu Phe Leu Ala His Arg Val Ala Leu Ala Ala Leu  
 368 1 5 10 15  
 370 Pro Cys Arg Arg Gly Ser Arg Gly Phe Gly Met Phe Tyr Ala Val Arg  
 371 20 25 30  
 373 Arg Gly Arg Lys Thr Gly Val Phe Leu Thr Trp Asn Glu Cys Arg Ala  
 374 35 40 45  
 376 Gln Val Asp Arg Phe Pro Ala Ala Arg Phe Lys Lys Phe Ala Thr Glu  
 377 50 55 60  
 379 Asp Glu Ala Trp Ala Phe Val Arg Lys Ser Ala Ser Pro Glu Val Ser  
 380 65 70 75 80  
 382 Glu Gly His Glu Asn Gln His Gly Gln Glu Ser Glu Ala Lys Pro Gly  
 383 85 90 95  
 385 Lys Arg Leu Arg Glu Pro Leu Asp Gly Asp Gly His Glu Ser Ala Gln  
 386 100 105 110  
 388 Pro Tyr Ala Lys His Met Lys Pro Ser Val Glu Pro Ala Pro Pro Val  
 389 115 120 125  
 391 Ser Arg Asp Thr Phe Ser Tyr Met Gly Asp Phe Val Val Val Tyr Thr  
 392 130 135 140  
 394 Asp Gly Cys Cys Ser Ser Asn Gly Arg Arg Lys Pro Arg Ala Gly Ile  
 395 145 150 155 160  
 397 Gly Val Tyr Trp Gly Pro Gly His Pro Leu Asn Val Gly Ile Arg Leu  
 398 165 170 175  
 400 Pro Gly Arg Gln Thr Asn Gln Arg Ala Glu Ile His Ala Ala Cys Lys  
 401 180 185 190  
 403 Ala Ile Glu Gln Ala Lys Thr Gln Asn Ile Asn Lys Leu Val Leu Tyr  
 404 195 200 205  
 406 Thr Asp Ser Met Phe Thr Ile Asn Gly Ile Thr Asn Trp Val Gln Gly  
 407 210 215 220  
 409 Trp Lys Lys Asn Gly Trp Lys Thr Ser Ala Gly Lys Glu Val Ile Asn  
 410 225 230 235 240

Do not enter <309> if you do  
 not have a <308> Database Accession  
 Number

<210> 13 Seg. #13

<211> 20

<212> DNA

<213> Artificial

<220>

<223> Sense primer

<400> 13

agcaggcgcc gcttcgaggc

20

<210> 14 Seg #14

<211> 26

<212> DNA

<213> Artificial

<220>

<223> Sense primer

<400> 14

cccgtcctg cagtattagt tcttgc

<210> 15 Seg #15

<211> 25

<212> DNA

<213> Artificial

<220>

<223> Sense primer

<400> 15

ttgcagctgg tgggtggcggc tgagg

25

Circled <213> responses are incomplete as per section 1.823b of the new sequence rules. See #11 on the Error Summary Sheet.

Note: This error occurs  
26  
throughout the sequence listing.  
please review and correct.



## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/781,712A

DATE: 05/17/2001

TIME: 10:13:23

Input Set : A:\es.txt

Output Set: N:\CRF3\05172001\I781712A.raw

L:355 M:286 W: Invalid Database Entry: Valid Formats YYYY-MM-DD or Mon-YYYY, SEQ ID:6  
L:357 M:284 W: Blank Line not Allowed, <310> field identifier  
L:908 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13  
L:926 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14  
L:945 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15  
L:963 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16  
L:981 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17  
L:999 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18  
L:1017 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19  
L:1035 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20  
L:1053 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21  
L:1071 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22  
L:1089 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23  
L:1107 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24  
L:1126 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25  
L:1144 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26  
L:1162 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:27  
L:1181 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:28  
L:1199 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:29  
L:1217 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:30  
L:1235 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:31  
L:1253 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:32  
L:1271 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:33  
L:1289 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:34  
L:1307 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:35  
L:1325 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:36  
L:1343 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:37  
L:1361 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:38  
L:1379 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:39